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01/18
10/15/2001

CRF Errors Corrected by the STIC Systems Branch

CRF Processing Date: 10/15/2001
Edited by: A
Verified by: A (STIC staff)

ENTERED

Serial Number: 09/746,783

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file;
☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form. 3/1/95

RAW SEQUENCE LISTING

DATE: 10/15/2001

PATENT APPLICATION: US/09/746,783

TIME: 21:07:52

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\10152001\I746783.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Jacobs, Kenneth

6 McCoy, John M.

7 LaVallie, Edward R.

8 Racie, Lisa A.

9 Treacy, Maurice

10 Spaulding, Vikki

11 Agostino, Michael J.

12 Howes, Steven H.

13 Fechtel, Kim

15 (ii) TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
16 ENCODING THEM

18 (iii) NUMBER OF SEQUENCES: 231

20 (iv) CORRESPONDENCE ADDRESS:

21 (A) ADDRESSEE: Genetics Institute, Inc.

22 (B) STREET: 87 CambridgePark Drive

23 (C) CITY: Cambridge

24 (D) STATE: MA

25 (E) COUNTRY: U.S.A.

26 (F) ZIP: 02140

28 (v) COMPUTER READABLE FORM:

29 (A) MEDIUM TYPE: Floppy disk

30 (B) COMPUTER: IBM PC compatible

31 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

32 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

34 (vi) CURRENT APPLICATION DATA:

C--> 35 (A) APPLICATION NUMBER: US/09/746,783

C--> 36 (B) FILING DATE: 21-Dec-2000

37 (C) CLASSIFICATION:

39 (viii) ATTORNEY/AGENT INFORMATION:

40 (A) NAME: Milasincic, Debra J.

41 (B) REGISTRATION NUMBER: 46,931

43 (ix) TELECOMMUNICATION INFORMATION:

44 (A) TELEPHONE: (617) 227-7400

45 (B) TELEFAX: (617) 742-4214

48 (2) INFORMATION FOR SEQ ID NO: 1:

50 (i) SEQUENCE CHARACTERISTICS:

51 (A) LENGTH: 2043 base pairs

52 (B) TYPE: nucleic acid

53 (C) STRANDEDNESS: double

54 (D) TOPOLOGY: linear

56 (ii) MOLECULE TYPE: cDNA

58 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

60	CTGAATGCCC CATGCGCACC CCACAGCTCG CGTCCTGCA AGTGTTCCTT CTGGTGTTC	60
62	CCGATGGCGT CCGGCCTCAG CCCTCTTCCT CCCCATCAGG GGCAGTGCCC ACGTCTTTGG	120
64	AGCTGCAGCG AGGGACGGAT GGCGGAACCC TCCAGTCCCC TTCAGAGGCG ACTGCAACTC	180

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66 GCCCGGCCGT GCCTGGACTC CCTACAGTGG TCCCTACTCT CGTGACTCCC TCGGCCCCCTG 240
68 GGAATAGGAC TGTGGACCTC TTCCCAGTCT TACCGATCTG TGTCTGTGAC TTGACTCCTG 300
70 GAGCCTGCGA TATAAATTGC TGCTGCGACA GGGACTGCTA TCTTCTCCAT CCGAGGACAG 360
72 TTTTCTCCTT CTGCCTTCCA GGCAGCGTAA GGTCTTCAAG CTGGGTTTGT GTAGACAAC 420
74 CTGTTATCTT CAGGAGTAAT TCCCCGTTTC CTTCAAGAGT TTTTCATGGAT TCTAATGGAA 480
76 TCAGGCAGTT TTGTGTCCAT GTGAACAAC CAAACTTAAA CTATTTCCAG AAGCTTCAAA 540
78 AGGTCAATGC AACCAACTTC CAGGCCCTGG TTGCAGAGTT TGGAGGCGAA TCATTCACTT 600
80 CAACATTCCA AACTCAATCA CCACCATCTT TTTACAGGGC CGGGGACCCC ATTCTTACTT 660
82 ACTTCCCCAA GTGGTCTGTA ATAAGCTTGC TGAGACAACC TGCAGGAGTT GGAGCTGGGG 720
84 GACTCTGTGC TGAAAGCAAT CCTGCAGGTT TCCTAGAGAG TAAAAGTACA ACTTGCACTC 780
86 GTTTTTTTCA AGAACCTGGC TAGTAGCTGT ACCTTGGAAT CAGCCCTCAA TGCTGCCTCT 840
88 TACTATAACT TCACAGTCTT AAAGGTTCCA AGAAGCATGA CTGATCCACA GAATATGGAG 900
90 TTCCAGGTTT CTGTAATACT TACCTCACAG GCTAATGCTC CTCTGTTGGC TGGAAACACT 960
92 TGTCAGAATG TAGTTTCTCA GGTCACCTAT GAGATAGAGA CCAATGGGAC TTTTGGAATC 1020
94 CAGAAAGTTT CTGTCAGTTT GGGACAAACC AACCTGACTG TTGAGCCAGG CGCTTCCTTA 1080
96 CAGCAACACT TCATCCTTCG CTTCAGGGCT TTTCAACAGA GCACAGCTGC TTCTCTCACC 1140
98 AGTCTAGAA GTGGGAATCC TGGCTATATA GTTGGGAAGC CACTCTTGGC TCTGACTGAT 1200
100 GATATAAGTT ACTCAATGAC CCTCTTACAG AGCCAGGGTA ATGGAAGTTG CTCTGTTAAA 1260
102 AGACATGAAG TGCAGTTTGG AGTGAATGCA ATATCTGGAT GCAAGCTCAG GTTGAAGAAG 1320
104 GCAGACTGCA GCCACTTGCA GCAGGAGATT TATCAGACTC TTCATGGAAG GCCCAGACCA 1380
106 GAGTATGTTG CCATCTTTGG TAATGCTGAC CCAGCCCAGA AAGGAGGGTG GACCAGGATC 1440
108 CTCAACAGGC ACTGCAGCAT TTCAGCTATA AACTGTACTT CCTGCTGTCT CATACCAGTT 1500
110 TCCCTGGAGA TCCAGGTATT GTGGGCATAT GTAGGTCTCC TGTCCAACCC GCAAGCTCAT 1560
112 GTATCAGGAG TTCGATTCTT ATACCAGTGC CAGTCTATAC AGGATTCTCA GCAAGTTACA 1620
114 GAAGTATCTT TGACAACTCT TGTGAACTTT GTGGACATTA CCCAGAAGCC ACAGCCTCCA 1680
116 AGGGGCCAAC CAAAATGGA CTGGAATGG CCATTCGACT TCTTCCCTT CAAAGTGGCA 1740
118 TTCAGCAGAG GAGTATTCTC TCAAAAATGC TCAGTCTCTC CCATCCTTAT CCTGTGCCTC 1800
120 TTAGAACTTG GAGTTCTCAA CCTAGAGACT ATGTGAAGAA AAGAAAATAA TCAGATTTC 1860
122 GTTTTCCCTA TGAGAACTC TGAGGCAGCC ACTTATCTTG GCTAAATAGA ACCTCACCTG 1920
124 CTCATGACCA GAGAGCATTT AGGATAATAG AGGACCTAAC TGAAGGAATC CTTGTATATG 1980
126 AAAGGAGTTA TTTTAGAAAA GCAATAAAAA TATTTTATTC ATCATAAAAA AAAAAAAAAA 2040
128 AAA 2043

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130 (2) INFORMATION FOR SEQ ID NO: 2:

132 (i) SEQUENCE CHARACTERISTICS:

133 (A) LENGTH: 263 amino acids

134 (B) TYPE: amino acid

135 (C) STRANDEDNESS:

136 (D) TOPOLOGY: linear

138 (ii) MOLECULE TYPE: protein

140 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

142 Met Arg Thr Pro Gln Leu Ala Leu Leu Gln Val Phe Phe Leu Val Phe
143 1 5 10 15
145 Pro Asp Gly Val Arg Pro Gln Pro Ser Ser Ser Pro Ser Gly Ala Val
146 20 25 30
148 Pro Thr Ser Leu Glu Leu Gln Arg Gly Thr Asp Gly Gly Thr Leu Gln
149 35 40 45
151 Ser Pro Ser Glu Ala Thr Ala Thr Arg Pro Ala Val Pro Gly Leu Pro
152 50 55 60
154 Thr Val Val Pro Thr Leu Val Thr Pro Ser Ala Pro Gly Asn Arg Thr

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155      65      70      75      80
157 Val Asp Leu Phe Pro Val Leu Pro Ile Cys Val Cys Asp Leu Thr Pro
158      85      90      95
160 Gly Ala Cys Asp Ile Asn Cys Cys Cys Asp Arg Asp Cys Tyr Leu Leu
161      100      105      110
163 His Pro Arg Thr Val Phe Ser Phe Cys Leu Pro Gly Ser Val Arg Ser
164      115      120      125
166 Ser Ser Trp Val Cys Val Asp Asn Ser Val Ile Phe Arg Ser Asn Ser
167      130      135      140
169 Pro Phe Pro Ser Arg Val Phe Met Asp Ser Asn Gly Ile Arg Gln Phe
170      145      150      155      160
172 Cys Val His Val Asn Asn Ser Asn Leu Asn Tyr Phe Gln Lys Leu Gln
173      165      170      175
175 Lys Val Asn Ala Thr Asn Phe Gln Ala Leu Val Ala Glu Phe Gly Gly
176      180      185      190
178 Glu Ser Phe Thr Ser Thr Phe Gln Thr Gln Ser Pro Pro Ser Phe Tyr
179      195      200      205
181 Arg Ala Gly Asp Pro Ile Leu Thr Tyr Phe Pro Lys Trp Ser Val Ile
182      210      215      220
184 Ser Leu Leu Arg Gln Pro Ala Gly Val Gly Ala Gly Gly Leu Cys Ala
185      225      230      235      240
187 Glu Ser Asn Pro Ala Gly Phe Leu Glu Ser Lys Ser Thr Thr Cys Thr
188      245      250      255
190 Arg Phe Phe Gln Glu Pro Gly
191      260
193 (2) INFORMATION FOR SEQ ID NO: 3:
195 (i) SEQUENCE CHARACTERISTICS:
196 (A) LENGTH: 1263 base pairs
197 (B) TYPE: nucleic acid
198 (C) STRANDEDNESS: double
199 (D) TOPOLOGY: linear
201 (ii) MOLECULE TYPE: cDNA
203 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
205 GAGCAGCTCA TCAACCCCTT TGGAGAGGAT GATGATGATT TTGAGACCAA CTGGATTGTC      60
207 GACAGGAATT TGCAGGTGTC CCTGTTGGCT GTGGATGAGA TGCACCAGGA CCTGCCTCGG      120
209 ATGGAGCCGG ACATGTACTG GAATAAGCCC GAGCCACAGC CCCCCTACAC AGCTGCTTCC      180
211 GCCCAGTTCC GTCGAGCCTC CTTTATGGGC TCCACCTTCA ACATCAGCCT GAACAAAGAG      240
213 GAGATGGAGT TCCAGCCCAA TCAGGAGGAC GAGGAGGATG CTCACGCTGG CATCATTGGC      300
215 CGCTTCCTAG GCCTGCAGTC CCATGATCAC CATCCTCCCA GGGCAAACCTC AAGGACCAAA      360
217 CTACTGTGGC CCAAGAGGGA ATCCCTTCTC CACGAGGGCC TGCCCCAAAA CCACAAGGCA      420
219 GCCAAACAGA ACGTTAGGGG CCAGGAAGAC AACAAAGCCT GGAAGCTTAA GGCTGTGGAC      480
221 GCCTTCAAGT CTGCCCCACT GTATCAGAGG CCAGGCTACT ACAGTGCCCC ACAGACGCCC      540
223 CTCAGCCCCA CTCCCATGTT CTTCCCCCTA GAACCATCAG CGCCGTCAAA GCTTCACAGT      600
225 GTCACAGGCA TAGACACCAA AGACAAAAGC TTAAAGACTG TGAGTTCTGG GGCCAAGAAA      660
227 AGTTTGAAT TGCTCTCAGA GAGCGATGGG GCCTTGATGG AGCACCAGCA AGTATCTCAA      720
229 GTGAGGAGGA AAAGTGTGGA GTTTAACCTG ACGGATATGC CAGAGATCCC CGAAAATCAC      780
231 CTCAAAGAAC CTTTGGAACA ATCACCACCC AACATACACA CTACACTCAA AGATCACATG      840
233 GATCCTTATT GGGCCTTGGA AAACAGGGAT GAAGCACATT CCTAACCTGC TTCCTAATGG      900
235 GGATGCTTCG CCAGCCAGGT CCTCACCTGT GTGTACACCA GCAGGACACT GATCCAGTCA      960

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237 CAGCCATACA GCTGTCCACA CTGAAGAACA TGTCTTACAA CAGCCTGAAT CAAATGGCTA      1020
239 GCTTAATAGA TAAAAATCCC AGACTACTTC AGCCTTTAAT GCCTTTTATT CATAAAAACT      1080
241 GTGAAAGCTA GACTGAACCA TTGGAACAT TTAAGTCAGA CTCTGGATTC AGAGTCGGGA      1140
243 ACCCTTAGTT CTATCTGAAT CCAAGACAGC CACACCTTAG TATACTGCCC AAATAATGA      1200
245 GTTTAATAAA TACAAATACT CGTTAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA      1260
247 AAA                                                                    1263
249 (2) INFORMATION FOR SEQ ID NO: 4:
251     (i) SEQUENCE CHARACTERISTICS:
252         (A) LENGTH: 261 amino acids
253         (B) TYPE: amino acid
254         (C) STRANDEDNESS:
255         (D) TOPOLOGY: linear
257     (ii) MOLECULE TYPE: protein
259     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
261 Met His Gln Asp Leu Pro Arg Met Glu Pro Asp Met Tyr Trp Asn Lys
262   1             5             10             15
264 Pro Glu Pro Gln Pro Pro Tyr Thr Ala Ala Ser Ala Gln Phe Arg Arg
265             20             25             30
267 Ala Ser Phe Met Gly Ser Thr Phe Asn Ile Ser Leu Asn Lys Glu Glu
268             35             40             45
270 Met Glu Phe Gln Pro Asn Gln Glu Asp Glu Glu Asp Ala His Ala Gly
271             50             55             60
273 Ile Ile Gly Arg Phe Leu Gly Leu Gln Ser His Asp His His Pro Pro
274             65             70             75             80
276 Arg Ala Asn Ser Arg Thr Lys Leu Leu Trp Pro Lys Arg Glu Ser Leu
277             85             90             95
279 Leu His Glu Gly Leu Pro Lys Asn His Lys Ala Ala Lys Gln Asn Val
280             100            105            110
282 Arg Gly Gln Glu Asp Asn Lys Ala Trp Lys Leu Lys Ala Val Asp Ala
283             115            120            125
285 Phe Lys Ser Ala Pro Leu Tyr Gln Arg Pro Gly Tyr Tyr Ser Ala Pro
286             130            135            140
288 Gln Thr Pro Leu Ser Pro Thr Pro Met Phe Phe Pro Leu Glu Pro Ser
289             145            150            155            160
291 Ala Pro Ser Lys Leu His Ser Val Thr Gly Ile Asp Thr Lys Asp Lys
292             165            170            175
294 Ser Leu Lys Thr Val Ser Ser Gly Ala Lys Lys Ser Phe Glu Leu Leu
295             180            185            190
297 Ser Glu Ser Asp Gly Ala Leu Met Glu His Pro Glu Val Ser Gln Val
298             195            200            205
300 Arg Arg Lys Thr Val Glu Phe Asn Leu Thr Asp Met Pro Glu Ile Pro
301             210            215            220
303 Glu Asn His Leu Lys Glu Pro Leu Glu Gln Ser Pro Thr Asn Ile His
304             225            230            235            240
306 Thr Thr Leu Lys Asp His Met Asp Pro Tyr Trp Ala Leu Glu Asn Arg
307             245            250            255
309 Asp Glu Ala His Ser
310             260
312 (2) INFORMATION FOR SEQ ID NO: 5:

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/746,783

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TIME: 21:07:52

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\10152001\I746783.raw

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314      (i) SEQUENCE CHARACTERISTICS:
315          (A) LENGTH: 894 base pairs
316          (B) TYPE: nucleic acid
317          (C) STRANDEDNESS: double
318          (D) TOPOLOGY: linear
320      (ii) MOLECULE TYPE: cDNA
322      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
324 CTTTGAGGGT TTTTGTGTTT TTGTTTTTTC TAGGATTTCa TTGTGATGTT TTGGTTTGTG      60
326 TTTTGTCTTT TTGTTTAAGT TGTGCTGACA CCAAACACAT CCAGTTTATA ATCAGTACAT      120
328 TGGAAAGCTG GTATTGATGT AGAACCAGTG CATAACTTTT TATGGGGTTT TGTTATTGGT      180
330 TTTTTTTTTG TAAAGTGTGA ATAAAAGGTA TGTTTACTCA TTTTTCCTGA ACACTGTGTT      240
332 GGTAATGTGC ATCATGACAA TTTCCAGTGA AGGTGAGCTG GAGCTGGTTG GACTAATGAG      300
334 ACTGAGGAAG CAGCTTTTCC TACGATCTGC ATTATGTAAT CACAGGTCCA GAGAGCTTTA      360
336 TGGAAGCGGG AGAGGAGGAG CACTTACTCA TGTTGTATTT GTTAATGGAG GATGTCATCT      420
338 TTTCATAGAT GCTGGAAC TA GAGTGCAC TT TAGATGCT AAAGGTTTGA GCTTTACACA      480
340 AAATGTCTTC ATCTGTATTT GTTATTGTCT ACAATATATT TGAATTTGGG GCAGCATATT      540
342 AAGATGTAAT GCCCTGTTAT GTCTGGAAAA AACTTGTTTT GCTTCTTCCA GGCAAAGGGC      600
344 ATTTTGTGGA TCAGTTTGAA CAGCTTCTCC ACCTTATTTG GACAGTGATA AATTGAACCA      660
346 AGAGTGTAGA TTTACAAGTG TAACCTTCAA AAGAGGAAGA ACTATTTGGG GTCTGTAGGT      720
348 AATGAACAGT CACACCAAAA TAGACTATGA TGCTTTTGTT AAGAAAGGTT TCATGTTTTA      780
350 GATATTTTCC GTGTCCTAAA TAATTTTCAA TAATCTATAA TCCCTAAAAT GCAATAAAAA      840
352 CTAGTATGTT TTCAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAA      894
354 (2) INFORMATION FOR SEQ ID NO: 6:
356      (i) SEQUENCE CHARACTERISTICS:
357          (A) LENGTH: 92 amino acids
358          (B) TYPE: amino acid
359          (C) STRANDEDNESS:
360          (D) TOPOLOGY: linear
362      (ii) MOLECULE TYPE: protein
364      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
366 Met Cys Ile Met Thr Ile Ser Ser Glu Gly Glu Leu Glu Leu Val Gly
367 1          5          10          15
369 Leu Met Arg Leu Arg Lys Gln Leu Phe Leu Arg Ser Ala Leu Cys Asn
370          20          25          30
372 His Arg Ser Arg Glu Leu Tyr Gly Ser Gly Arg Gly Gly Ala Leu Thr
373          35          40          45
375 His Val Val Phe Val Asn Gly Gly Cys His Leu Phe Ile Asp Ala Gly
376          50          55          60
378 Thr Arg Val His Leu Leu Asp Ala Lys Gly Leu Ser Phe Thr Gln Asn
379          65          70          75          80
381 Val Phe Ile Cys Ile Cys Tyr Cys Leu Gln Tyr Ile
382          85          90
384 (2) INFORMATION FOR SEQ ID NO: 7:
386      (i) SEQUENCE CHARACTERISTICS:
387          (A) LENGTH: 784 base pairs
388          (B) TYPE: nucleic acid
389          (C) STRANDEDNESS: double
390          (D) TOPOLOGY: linear
392      (ii) MOLECULE TYPE: cDNA

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/746,783

DATE: 10/15/2001

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Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\10152001\I746783.raw

L:35 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:36 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:2339 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48
L:2348 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48
L:3353 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:70
L:3356 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:70
L:3455 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:70
L:3670 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:74
L:3673 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:74
L:3807 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76
L:4611 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:86
L:5732 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:116
L:5741 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:116
L:7227 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:148
L:7230 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:148